Response dated May 19, 2008 Application No.: 10/632,099 Reply to Office Action dated November 19, 2007

In the Claims

- (Currently Amended) A method for identifying a drug discovery target <u>comprising</u> which comprises:
- (a) providing a means <u>computer</u> for <u>storing and</u> accessing genomics information <u>comprising</u> [[in]] a database wherein said <u>means computer</u> permits computational analysis of biological relationships among the stored concepts genomics information;
- (b) querying the database to identify a disease-related pathway-generating one or more subsets of genomics information from the database wherein at least one of the one or more subsets is a-disease-related pathway; and
- (c) identifying the biological <u>objects and processes that act on those objects interactions</u>

 and actor concepts in the disease-related pathway whereby each <u>object or process</u> involved in <u>the</u>

 disease-related pathway each such reaction is a drug discovery target; and
 - (d) accessing the drug discovery targets.
- (Currently Amended) The method of claim 1 wherein the genomics information comprises
 information relating to genes, their DNA sequences, mRNA, the proteins that result when the genes
 are expressed proteins expressed from said genes, and the biological effects of the expressed
 proteins.
- (Currently Amended) The method of claim 2 wherein the data said genomics information comprise data extracted from multiple public sources.
- (Currently Amended) The method of claim 2 wherein the data said genomics information comprises proprietary data.
- (Currently Amended) The method of claim 2 wherein the data said genomics information comprises data extracted from a combination of proprietary and public data sources.
- (Cancelled)

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- 7. (Original) The method of claim 2 wherein the means for storing the genomics information includes an ontology in which:
- (a) each gene, gene product, and biological effect is given an identifier which is related to synonyms for the identifier:
 - (b) each gene, gene product, and biological effect is categorized by class; and
- (c) the relationship of each gene, gene product and disease state is defined by slots and facets.
- (Currently Amended) The method of claim 2 wherein the eandidate drug discovery targets in
 the disease related pathway are prioritized based on factors that include function and complexity.
- (Currently Amended) The method of claim 8 wherein the eandidate drug discovery targets are further prioritized based on markers for side effects and patient responsiveness.

10-12. (Cancelled)

- 13. (Currently Amended) The method of claim 1 wherein the genomics information comprises information relating to genotype and the disease-related pathway comprises a gene, mRNA or protein expressed from said gene product associated with a particular genotype.
- 14. (Currently Amended) The method of claim 1 wherein the genomics information comprises the name of each gene, mRNA or <u>protein expressed from said gene product</u>, and their biological effects, and the means for storing and accessing the genomics information identifies relationships <u>between genes and/or proteins expressed from said genes</u> that are at least one two steps removed from each other in a disease-related pathway.

15-31. (Cancelled)

32-56. (Cancelled)

 (Currently Amended) A method for identifying a drug discovery target which comprises comprising: Response dated May 19, 2008 Application No.: 10/632,099 Reply to Office Action dated November 19, 2007

- (a) querying one or more subsets of genomics information generated from a database to identify:
 - (i) a disease-related pathway;
- (ii) the biological <u>objects and processes that act on those objects interactions and actor</u>
 eoneepts in the disease-related pathway, whereby at least one of the <u>object or processes</u> actor
 eoneepts involved in <u>each such reaction the disease-related pathway</u> is a drug discovery target and
 wherein the one or more subsets reside on a computer system <u>that allows eomprising a means for the</u>
 accessing <u>of genomics information stored</u> in the database and a <u>means for the performing of</u>
 computational analysis of biological relationships among the concepts contained within the subsets;
 and
- (b) accessing the results.
- 58-61. (Cancelled)